```
   1 GAATTCCGGCGCGGAGGCCGAGAGAGAAGTCACTTGCCCTGGCTCTACCTTGAAGTGGTTCTCAGGGTTGGGGCGAGAGTCGGGGTGGGGACCGAGATGC

 101 AGCTCTATCCTGTGCCCCTGGTCGCAGCAGGCAGCCCAGCGCTTCGCGTGTTCTACTTGGCCTGTCCGCTGCCGCCTAATGAGCTCAGGTCTAGGCCGAG

 201 CAGAGGGGGCACCTGGTCGGACTCGGTTGGGCTCGGGCGGCCCCGCCTCCCCCCGCCCGCCAGGCGGGCCCTTCTCGACGGCGCGGGGCGGGCCCTGCGG

 301 GCGCGGGGCTGAAGGCGGAACCACGACGGGCAGAGAGCACGGAGCCGGGAAGCCCCTGGGCGCCCGTCGGAGGGCTATGGAGCAGCGGCCGCGGGGCTGC
   1                                                                                   M  E  Q  R  P  R  G  C

 401 GCGGCGGTGGCGGCGGCGCTCCTCCTGGTGCTGCTGGGGGCCCGGGCCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGA
   9 A  A  V  A  A  A  L  L  L  V  L  L  G  A  R  A  Q  G  G  T  R  S  P  R  C  D  C  A  G  D  F  H  K  K

 501 AGATTGGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCTTGCACGGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGTCCCCA
  43   I  G  L  F  C  C  R  G  C  P  A  G  H  Y  L  K  A  P  C  T  E  P  C  G  N  S  T  C  L  V  C  P  Q

 601 AGACACCTTCTTGGCCTGGGAGAACCACCATAATTCTGAATGTGCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGCGCTGGAGAACTGTTCA
  76  D  T  F  L  A  W  E  N  H  H  N  S  E  C  A  R  C  Q  A  C  D  E  Q  A  S  Q  V  A  L  E  N  C  S

 701 GCAGTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGTGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTGCCAACCATGCC
 109 A  V  A  D  T  R  C  G  C  K  P  G  W  F  V  E  C  Q  V  S  Q  C  V  S  S  S  P  F  Y  C  Q  P  C  L

 801 TAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGCGATGG
 143   D  C  G  A  L  H  R  H  T  R  L  L  C  S  R  R  D  T  D  C  G  T  C  L  P  G  F  Y  E  H  G  D  G

 901 CTGCGTGTCCTGCCCCACGTAATTCCTAGCTGTCGTGGGATGGAGGGAAGGGCGGCTGGGAGCAGAGCAGGGGCCTGGGGTGGGGCAGGTGCTGCTGGTT
 176  C  V  S  C  P  T

1001 CAGGAATAGGAAGAGGGGATAGGGAGGAGGGAGCCTTGGCCCTGTGATGGGTGGGCCCCACTTCAGGCAAACTTAGATGGCAAAAGAGCAATCTGGATCC

1101 GCCTTAGCCAGATACATAAGGGTATTTGCCTTCACTTTCAGCCAGCATTCCCCCCAGCGATCCTAGCCAGATATTACAGATGATTTGTCACTTACACAGA

1201 GAGTCACATTGATATAGCTTTAAAACTTGGGCTGAAGGAGGTTGAGGCTGCAGTGAGCTATGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCGAG

1301 ACCTATTAAATAAATAAATAAATATTAAATCTATTAAATATTAAATATTAAATCTATTAAATAAATAAATACAAAGGGCTGAGAGTCAGGACTGTGCTGC

1401 TAGTTCTCTAGGGGATCTTGGGCAAGTGCAGAGAATTC
```

FIG. 1

#5

```
hApo2LI    34  D C A G D - - - - F H K K I G L F C C R G C P A G H Y L K A P C T E P C G N S T C L - - - - - - - - -
hTNFR1     43  V C P Q G K - - Y I H P Q N N S I C C T K C H K G T Y L Y N D C P G P G Q D T D C R - - - - - - - - -
hTNFR2     39  T C R L R E - - - Y Y D Q T A Q M C C S K C S P G Q H A K V F C T K T - S D T V C D - - - - - - - - -
hTNFRrp    42  T C R D Q E K E - Y Y E P Q H R I C C S R C P P G T Y V S A K C S R I - R D T V C A - - - - - - - - -
hFAS/Apo1  48  N L E G L - - - - - - H H D G Q F C H K P C P P G E R K A R D C T V N G D E P D C V - - - - - - - - -
hLNGFR     31  A C P T G - - - - - L Y T H S G E C C K A C N L G E G V A Q P C G A - - N Q T V C E - - - - - - - - -
hCD40      25  A C R E K - - - - - Q Y L I N S Q C C S L C Q P G Q K L V S D C T E F - T E T E C L - - - - - - - - -
hCD27      26  S C P E R - - - - H Y W A Q G K L C C Q M C E P G T F L V K D C D Q H R K A A Q C D - - - - - - - - -
hCD30      28  T C H G N P S H - Y Y D K A V R R C C Y R C P M G L F P T Q Q C P Q R - - P T D C R K - - - - - - - -
hOX40      30  H C V G D T - - - - - Y P S N D R C C H E C R P G N G M V S R C S R S - Q N T V C R - - - - - - - - -

hApo2LI    72  V C P Q D - T F L A W E N H H S E C A R C - Q A C D E Q A S Q V A L E N C S A V A D T R C G - - - -
hTNFR1     83  E C E S G - S F T A S E N H L R H C L S C - S K C R K E M G Q V E I S S C T V D R D T V C G - - - -
hTNFR2     77  S C E D S T Y T Q L W N W V - P E C L S C G S R C S S - - D Q V E T Q A C T R E Q N R I C T - - - -
hTNFRrp    82  T C A E N S Y N E H W N Y L - T I C Q L C - R P C D P V M G L E E I A P C T S K R K T Q C R - - - -
hFAS/Apo1  84  P C Q E G K E Y T D K A H F S S K C R R C - R L C D E G H G L E V E I N C T R T Q N T K C R - - - -
hLNGFR     66  P C L D S V T F S D V V S A T E P C K P C - T E C V G L - - Q S M S A P C V E A D D A V C R - - - -
hCD40      61  P C G E S E F L D T W N R E - T H C H Q H - K Y C D P N L G L R V Q Q K G T S E T D T I C T - - - -
hCD27      64  P C I P G V S F S P D H H T R P H C E S C - R H C N S G L L V R - - - N C T I T A N A E C A - - - -
hCD30      68  Q C E P D - Y Y L D E A D R - - - C T A C - V T C S R D D L V E K T - P C A W N S S R V C E - - - -
hOX40      66  P C G P G - F Y N D V V S S K P - C K P C - T W C N L R S G S E R K Q L C T A T Q D T V C R - - - -
```

FIG. 2A

```
hApo2LI   116 C K P G W F V E C Q V S Q C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R R D - T D C G - T
hTNFR1    127 C R K N Q Y R H Y W S E N L - - - - - F Q C F N C S L C L N G - - T V H L S C Q E K Q N T V C - - T
hTNFR2    120 C R P G W Y C A L S K Q E G C - - - - R L C A P L R K C R P G - F G V A R P G T E T S D V V C K - P
hTNFRrp   126 C Q P G M F C A A W A L E C - - - - - T H C E L L S D C P P G T E A E L K D E V G K G N N H C V - P
hFAS/Apo1 129 C K P N F F - - C N S T V C - - - - - E H C D P C T K C E H G I - - - I K E C T L T S N T K C K -
hLNGFR    109 C A Y G Y Y Q D E T T - - - - - - - - G R C E A C R V C E A G S G L - V F S C Q D K Q N T V C E - E
hCD40     105 C E E G W H C T S E A C - - - - - - - E S C V L H R S C S P G F G - V K Q I A T G V S D T I C E - P
hCD27     106 C R N G W Q C R D K E C - - - - - - - T E C D P L P N P S L T A R S S Q A L S P H P Q P T H L P -
hCD30     108 - C R P G M F C S T S A V N S C - - - - A R C F F H S V C P A G M I V K F P G T A Q K - N T V C E -
hOX40     109 - C R A G T Q P L D S Y K P G - - - - - V D C A - - - - - - - - - - - - - - - - - - - - - - - - -

hApo2LI   164 C L P G F Y E H G D - - - - G C V S C P T
hTNFR1    168 C H A G F F L R E N - - - - E C V S C S N C K K - - - - S L E C T K - - - - - L C L
hTNFR2    164 C A P G T F S N T T S S T D I C R P H Q I C N V V A I P G N A S M - - - - D A V C T
hTNFRrp   170 C K A G H F Q N T S S P S A R C Q P H T R C E N Q G L V E A A P G T A Q S D T T C K
hLNGFR    149 C P D G T Y S D E A N H V D P C L P C T V C E D T E R Q L R E C T R W - A D A E C E
hCD40     146 C P V G F F S N V S S A F E K C H P W T S C E T K D L V V Q Q A G T N K T D V V C G
hOX40     127 P C P P G H F S P G D - - N Q A C K P W T N C T L A G K H T L Q P A S N S S D A I C E
```

FIG. 2B

```
1081 GGGCCCGCAG CTCTACGACG TGATGGACGC GGTCCCAGCG CGGCGCTGGA AGGAGTTCGT
 332  G  P  Q   L  Y  D  V  M  D  A  V  P  A  R  R  W  K  E  F  V

1141 GCGCACGCTG GGGCTGCGCG AGGCAGAGAT CGAAGCCGTG GAGGTGGAGA TCGGCCGCTT
 352  R  T  L  G  L  R  E  A  E  I  E  A  V  E  V  E  I  G  R  F

1201 CCGAGACCAG CAGTACGAGA TGCTCAAGCG CTGGCGCCAG CAGCAGCCCG CGGGCCTCGG
 372  R  D  Q  Q  Y  E  M  L  K  R  W  R  Q  Q  Q  P  A  G  L  G

1261 AGCCGTTTAC GCGGCCCTGG AGCGCATGGG GCTGGACGGC TGCGTGGAAG ACTTGCGCAG
 392  A  V  Y  A  A  L  E  R  M  G  L  D  G  C  V  E  D  L  R  S

1321 CCGCCTGCAG CGCGGCCCGT GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC
 412  R  L  Q  R  G  P

1381 TTGCAGAAGC CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC

1441 CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC CCCTATCGCT

1501 CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG GTGAAGACAT TTCTCAACTT

1561 CTCGGCCGGA GTTTGGCTGA GATCGCGGTA TTAAATCTGT GAAAGAAAAC AAAAAAAAAA

1621 AAAAAAAAAA AAAA
```

FIG. 4C

```
541 ACGGCTACTC TGTTCCCGCA GAGATACTGA CTGTGGGACC TGCCTGCCTG GCTTCTATGA
152   R   L   L     C   S   R   R     D   T   D     C   G   T     C   L   P   G     F   Y   E

601 ACATGGCGAT GGCTGCGTGT CCTGCCCCAC GAGCACCCTG GGGAGCTGTC CAGAGCGCTG
172   H   G   D     G   C   V   S     C   P   T     S   T   L     G   S   C   P     E   R   C

661 TGCCGCTGTC TGTGGCTGGA GGCAGATGTT CTGGGTCCAG GTGCTCCTGG CTGGCCTTGT
192   A   A   V     C   G   W   R     Q   M   F     W   V   Q     V   L   L   A     G   L   V

721 GGTCCCCCTC CTGCTTGGGG CCACCCTGAC CTACACATAC CGCCACTGCT GGCCTCACAA
212   V   P   L     L   L   G   A     T   L   T     Y   T   Y     R   H   C   W     P   H   K

781 GCCCCTGGTT ACTGCAGATG AAGCTGGGAT GGAGGCTCTG ACCCCACCAC CGGCCACCCA
232   P   L   V     T   A   D   E     A   G   M     E   A   L     T   P   P   P     A   T   H

841 TCTGTCACCC TTGGACAGCG CCCACACCCT TCTAGCACCT CCTGACAGCA GTGAGAAGAT
252   L   S   P     L   D   S   A     H   T   L     L   A   P     P   D   S   S     E   K   I

901 CTGCACCGTC CAGTTGGTGG GTAACAGCTG GACCCCTGGC TACCCCGAGA CCCAGGAGGC
272   C   T   V     Q   L   V   G     N   S   W     T   P   G     Y   P   E   T     Q   E   A

961 GCTCTGCCCG CAGGTGACAT GGTCCTGGGA CCAGTTGCCC AGCAGAGCTC TTGGCCCCGC
292   L   C   P     Q   V   T   W     S   W   D     Q   L   P     S   R   A   L     G   P   A

1021 TGCTGCGCCC ACACTCTCGC CAGAGTCCCC AGCCGGCTCG CCAGCCATGA TGCTGCAGCC
312   A   A   P     T   L   S   P     E   S   P     A   G   S     P   A   M   M     L   Q   P
```

FIG. 4B

```
   1 CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GCAGAGAGC ACGGAGCCGG

  61 GAAGCCCCTG GGCGCCCGTC GGAGGGCTAT GGAGCAGCGG CCGCGGGGCT GCGCGGCGGT
   1                                  M  E  Q  R  P  R  G  C  A  A  V

 121 GGCGGCGGCG CTCCTCCTGG TGCTGCTGGG GGCCCGGGCC CAGGGCGGCA CTCGTAGCCC
  12  A  A  A  L  L  L  V  L  L  G  A  R  A  Q  G  G  T  R  S  P

 181 CAGGTGTGAC TGTGCCGGTG ACTTCCACAA GAAGATTGGT CTGTTTTGTT GCAGAGGCTG
  32  R  C  D  C  A  G  D  F  H  K  K  I  G  L  F  C  C  R  G  C

 241 CCCAGCGGGG CACTACCTGA AGGCCCCTTG CACGGAGCCC TGCGGCAACT CCACCTGCCT
  52  P  A  G  H  Y  L  K  A  P  C  T  E  P  C  G  N  S  T  C  L
                                                 *

 301 TGTGTGTCCC CAAGACACCT TCTTGGCCTG GGAGAACCAC CATAATTCTG AATGTGCCCG
  72  V  C  P  Q  D  T  F  L  A  W  E  N  H  H  N  S  E  C  A  R

 361 CTGCCAGGCC TGTGATGAGC AGGCCTCCCA GGTGGCGCTG GAGAACTGTT CAGCAGTGGC
  92  C  Q  A  C  D  E  Q  A  S  Q  V  A  L  E  N  C  S  A  V  A
                                                 *

 421 CGACACCCGC TGTGGCTGTA AGCCAGGCTG GTTTGTGGAG TGCCAGGTCA GCCAATGTGT
 112  D  T  R  C  G  C  K  P  G  W  F  V  E  C  Q  V  S  Q  C  V

 481 CAGCAGTTCA CCCTTCTACT GCCAACCATG CCTAGACTGC GGGGCCCTGC ACCGCCACAC
 132  S  S  S  P  F  Y  C  Q  P  C  L  D  C  G  A  L  H  R  H  T
```

FIG. 4A

```
Apo3          1  MEQRPRGCAAVAAAALLLVLLGARAQGGTRSPR------------
TNFR1         1  MGLSTVPDLLLPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV
Fas/Apo1      1  MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV

Apo3         33  CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLV
TNFR1        44  CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRE
Fas/Apo1     45  ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVP

Apo3         73  CPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG
TNFR1        85  CESGSFTASENHLRH-CLSCSKCRKEMGQVEISSCTVDRDTVCG
Fas/Apo1     85  CQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCR

Apo3        117  CKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRD-TDCGT
TNFR1       127  CRKNQYRHYWSENLFQ-----CFNCSLCLNGTVHLS--CQEKQNTVCT-
Fas/Apo1    129  CKPNFF--CNSTVCEH-----CDPCTKCEHGIIKE---CTLTSNTKCKE

Apo3        165  CLPGFYEHGDGCVSCPTSTLGSCP--ERCAAVCGW
TNFR1       168  CHAGFFLRENECVSCS-----NCKKSLECTKLCLP
```

FIG. 5

```
Apo3        338  VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR--FRDQQYE
TNFR1       333  VVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR-CLREAQYS
Fas/Apo1    220  IAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKV-Q
FADD        104  ICDNVGK-DWRRLARQLKVSDTKIDSIEDRYPRN-LTERVRE
TRADD       211  NRPLSLK-DQQTFARSVGLKWRKVGR-SLQRGCRALRDPALD
RIP         291  IRENLGK-HWKNCARKLGFTQSAIDEIDHDYERDGLKEKVYQ
Reaper        1                MAVAFYIPDQATLLREAEQKEQQILR-LRESQWR

Apo3        378  MLKRWRQQQP---AGLGAVYAALERMGL-DGCVEDLRS
TNFR1       374  MLATWRRRTPRREATLELLGRVLRDMDL-LGCLEDIEE
Fas/Apo1    261  LLRNWHQLHG-KKEAYDTLIKDLKKANLCTLA-EKIQT
FADD        144  SLRIWKNTE-KENATVAHLVGALRSC---QMNLVADLV
TRADD       251  SLAYEYEREGLYEQAFQLLRRFV-QAEGRRATLQRLVE
RIP         332  MLQKWVMREGIKGATVGKLAQALHQC--SRIDLLSSLT
Reaper        34 FLATVVLETLKQYTSCHPKTGRKSGKYRKP
```

FIG. 6

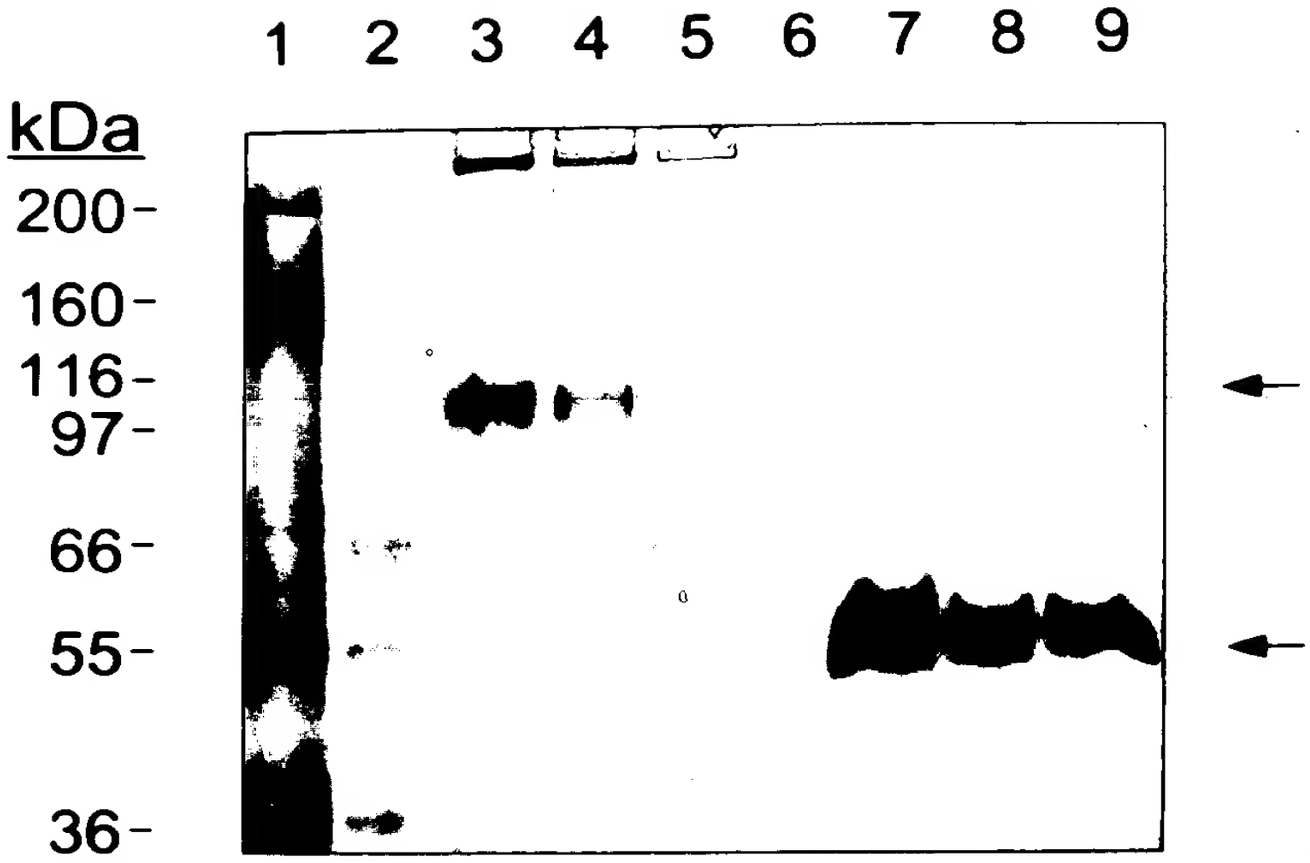


FIG. 3

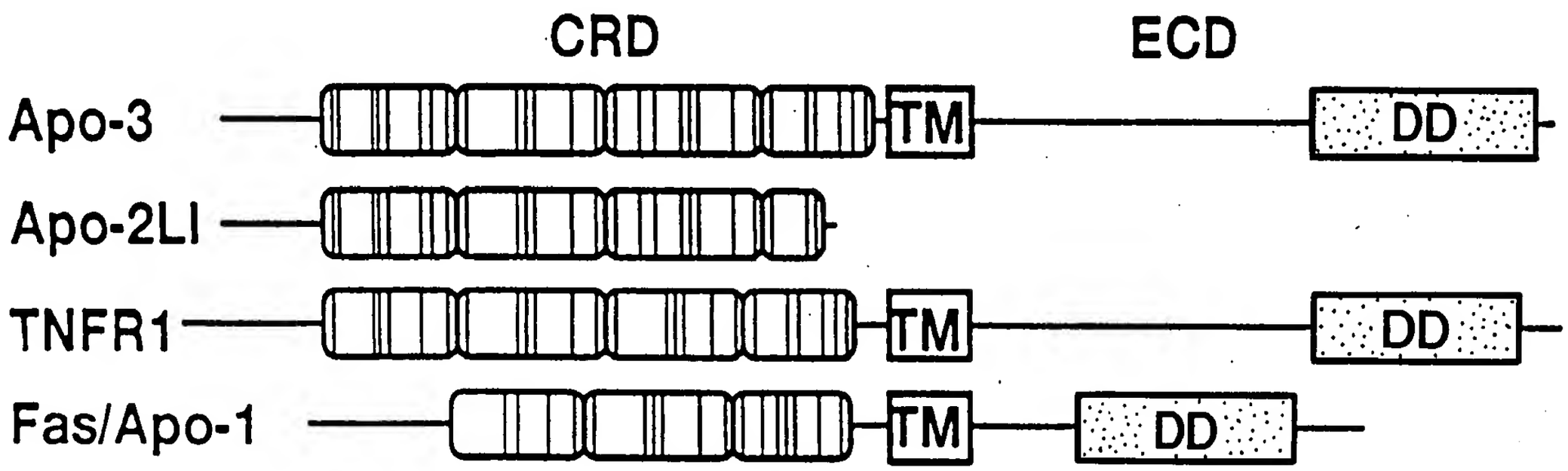


FIG. 7

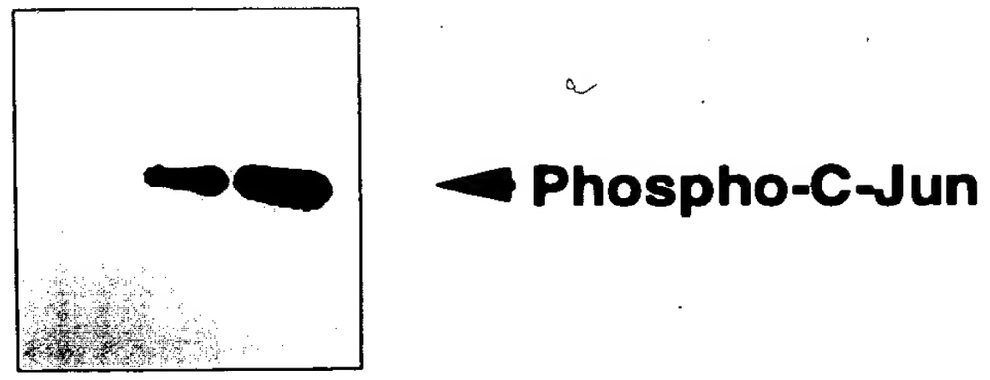

Transfection
pRK5
TNFR1
Apo-3
Phospho-C-Jun

FIG. 11

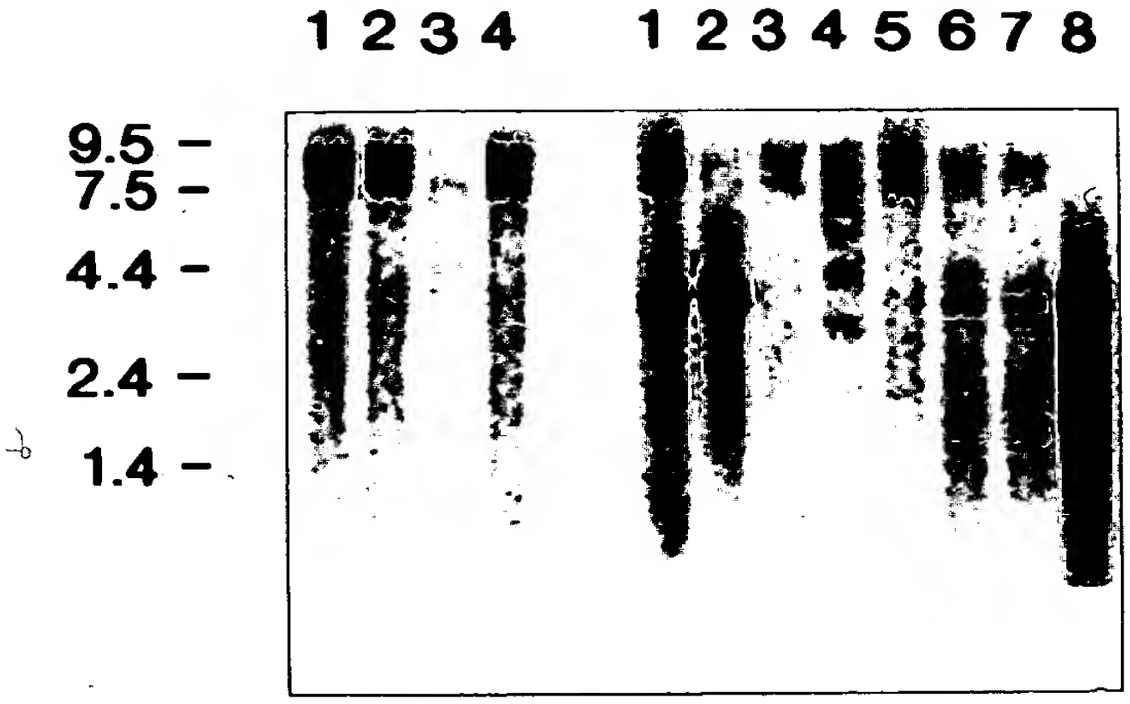

1 2 3 4
1 2 3 4 5 6 7 8
9.5
7.5
4.4
2.4
1.4

FIG. 12

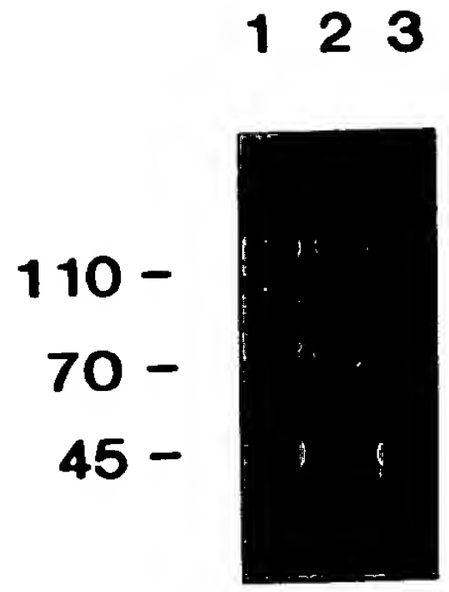


FIG. 8

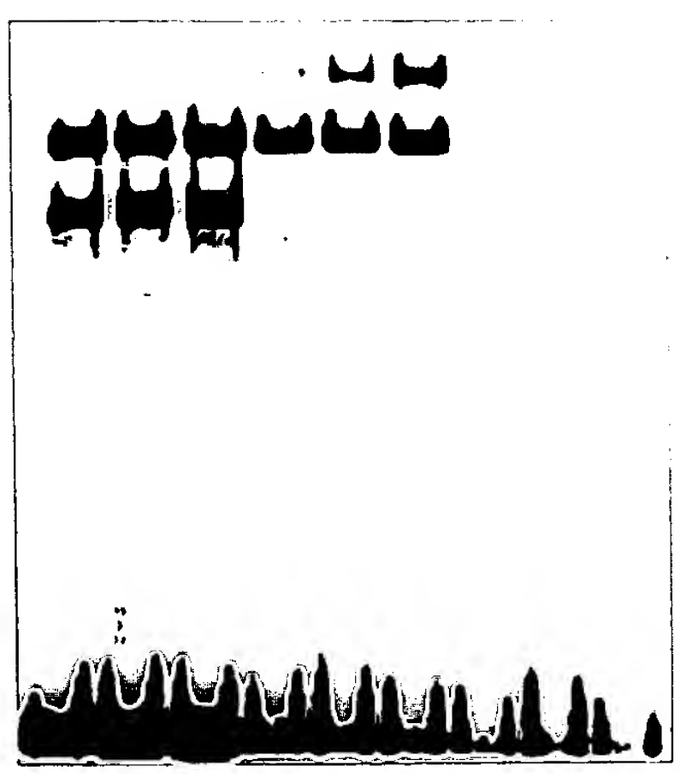


FIG. 10

FIG. 9A

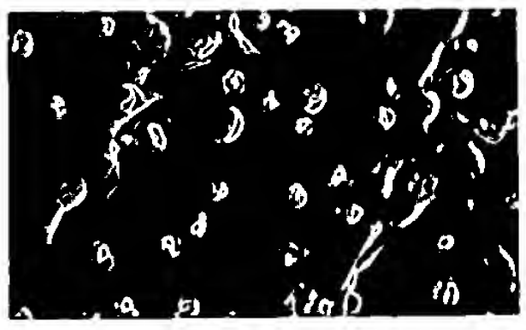
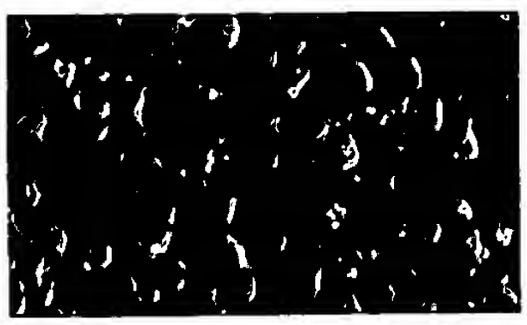


FIG. 9B

FIG. 9C



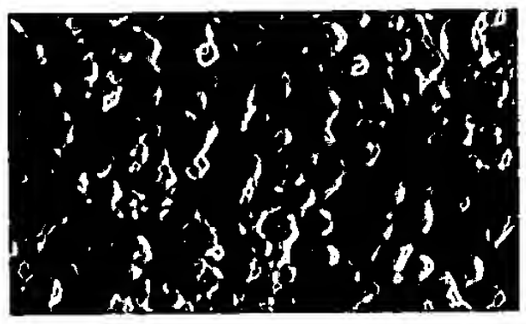
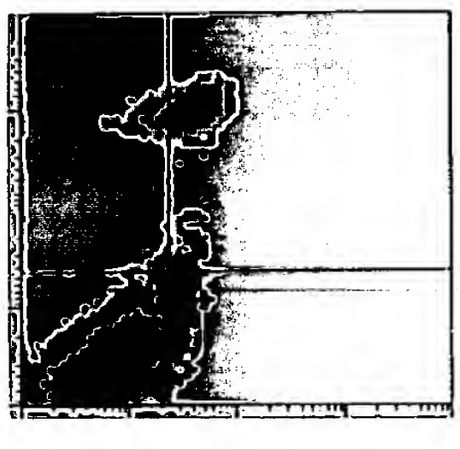


FIG. 9D

FIG. 9E



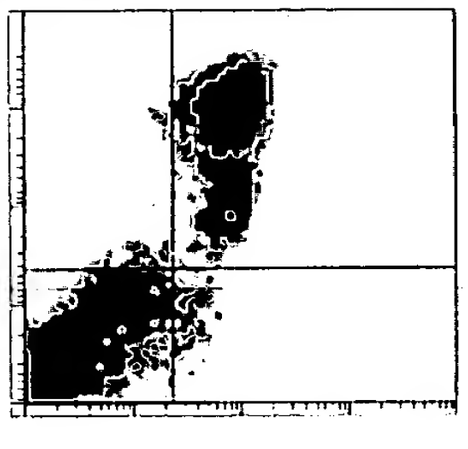
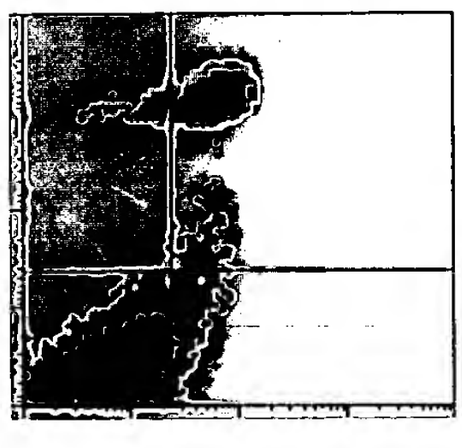


FIG. 9F

FIG. 9G



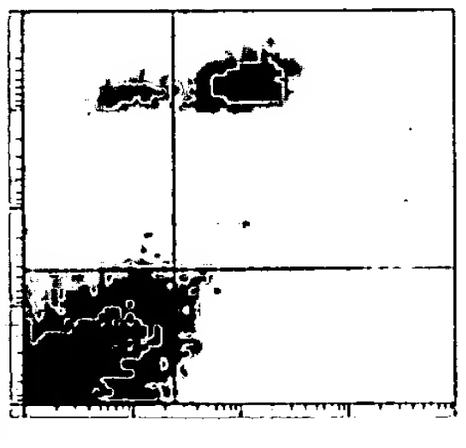


FIG. 9H

FIG. 9I

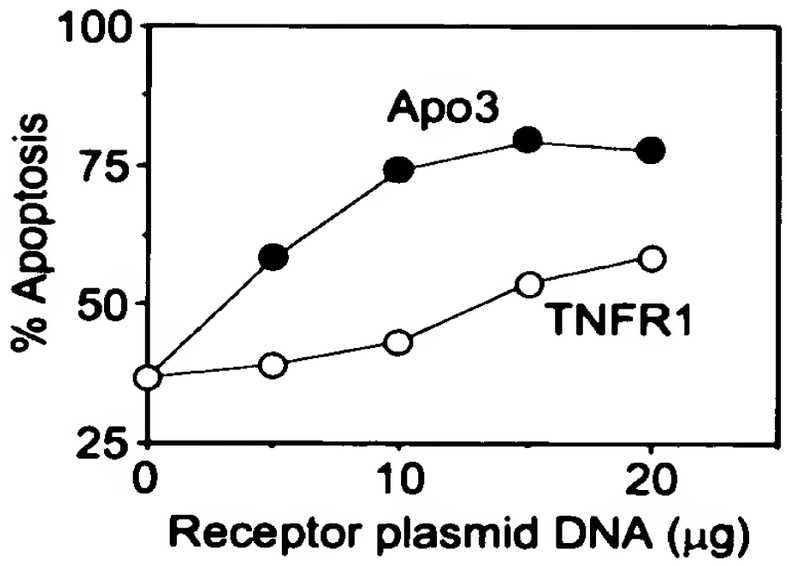


FIG. 9J